Amendments to the claims:

This listing of claims will replace all prior versions, and listings, of claims in the application:

Listing of claims:

1. (Currently Amended) A method for melanoma prognosis, comprising:

(a) isolating nucleic acid from a ~~biological~~ sentinel lymph node (SLN) sample obtained from a melanoma patient~~, wherein the biological sample is associated with melanoma~~;

(b) amplifying nucleic acid targets from a panel of marker genes, wherein the panel comprises GalNAcT, PAX3, or both;

(c) detecting the levels of the nucleic acid targets; and

(d) predicting melanoma recurrence, disease-free survival, overall survival, or a combination thereof, based on the levels of the nucleic acid targets, wherein, as compared to control levels, an increase in the levels of the nucleic acid targets is indicative of an increase in melanoma recurrence, a decrease in disease-free survival, or a decrease in overall survival, and a decrease in the levels of the nucleic acid targets is indicative of a decrease in melanoma recurrence, an increase in disease-free survival, or an increase in overall survival.

2. (Previously Presented) The method of claim 1 wherein the panel further comprises marker genes selected from a group consisting of MAGE-A3, MART-1, and Tyrosinase.

3. (Previously Presented) The method of claim 2 wherein the panel comprises a first combination of MAGE-A3, GalNAcT, MART-1, and PAX3; or a second combination of Tyrosinase, MART-1, GalNAcT, and PAX3.

4. (Original) The method of claim 1 wherein the nucleic acid is mRNA and the nucleic acid targets are amplified using real-time reverse transcriptase polymerase chain reaction (qRT-PCR).

5. (Currently Amended) The method of claim 1 wherein the ~~biological~~ SLN sample is ~~selected from a group consisting of~~ paraffin-embedded (PE) ~~melanoma tissues,~~ or frozen ~~lymph nodes, and PE lymph nodes~~.

6. (Currently Amended) The method of claim 1, wherein the ~~biological~~ SLN sample is histopathologically negative for melanoma cells.

7. (Currently Amended) The method of claim 6, wherein histopathology of the ~~biological~~ SLN sample is determined by hematoxylin and eosin staining or immunohistochemistry.

8-9. (Canceled)

10. (Previously Presented) The method of claim 1, wherein the patient's prognosis is predicted for at least a three-year period following a removal of a primary tumor, sentinel lymphadenectomy (SLND), or both.

11-30. (Canceled)

31. (Previously Presented) A method for detecting the expression of a panel of marker genes in a patient, comprising:

(a) obtaining a sentinel lymph node (SLN) sample from a melanoma patient, wherein the sample is histopathologically negative for melanoma cells;

(b) isolating nucleic acid from the sample;

(c) amplifying nucleic acid targets from a panel of marker genes, wherein the panel comprises GalNAcT, PAX3, or both; and

(d) detecting the levels of the nucleic acid targets.

32. (Previously Presented) The method of claim 31 wherein the panel further comprises marker genes selected from a group consisting of MAGE-A3, MART-1, and Tyrosinase.

33. (Previously Presented) The method of claim 32 wherein the panel comprises a first combination of MAGE-A3, GalNAcT, MART-1, and PAX3; or a second combination of Tyrosinase, MART-1, GalNAcT, and PAX3.

34. (New) A method for melanoma prognosis, comprising:

(a) isolating nucleic acid from a blood sample obtained from a melanoma patient;

(b) amplifying nucleic acid targets from a panel of marker genes, wherein the panel comprises GalNAcT, PAX3, or both;

(c) detecting the levels of the nucleic acid targets; and

(d) predicting melanoma recurrence, disease-free survival, overall survival, or a combination thereof, based on the levels of the nucleic acid targets, wherein, as compared to control levels, an increase in the levels of the nucleic acid targets is indicative of an increase in melanoma recurrence, a decrease in disease-free survival, or a decrease in overall survival, and a decrease in the levels of the nucleic acid targets is indicative of a decrease in melanoma recurrence, an increase in disease-free survival, or an increase in overall survival.

35. (New) A method for melanoma prognosis, comprising:

(a) isolating nucleic acid from a non-sentinel lymph node (NSLN) sample obtained from a melanoma patient;

(b) amplifying nucleic acid targets from a panel of marker genes, wherein the panel comprises GalNAcT, PAX3, or both;

(c) detecting the levels of the nucleic acid targets; and

(d) predicting melanoma recurrence, disease-free survival, overall survival, or a combination thereof, based on the levels of the nucleic acid targets, wherein, as compared to control levels, an increase in the levels of the nucleic acid targets is indicative of an increase in melanoma recurrence, a decrease in disease-free survival, or a decrease in overall survival, and a decrease in the levels of the nucleic acid targets is indicative of a decrease in melanoma recurrence, an increase in disease-free survival, or an increase in overall survival.